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Please remove extra information, "PF-1618 PCT" and "1?2", at the end of the file, after SEQ ID # 42.

Application No: 10534579 Version No: 1.0

Input Set:

Output Set:

Started: 2009-01-15 09:49:04.675
Finished: 2009-01-15 09:49:08.647
Elapsed: 0 hr(s) 0 min(s) 3 sec(s) 972 ms
Total Warnings: 0
Total Errors: 1
No. of SeqIDs Defined: 42
Actual SeqID Count: 42

Error code	Error Description
E 330	Invalid protein , found in SEQID(42) POS (1) Invalid Protein:PCT

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<120> TITLE OF INVENTION: LIPID-ASSOCIATED MOLECULES

<130> FILE REFERENCE: PF-1618 PCT

<140> CURRENT APPLICATION NUMBER:10534579
<141> CURRENT FILING DATE:2006-11-14
<150> PRIOR APPLICATION NUMBER: US 60/426,105
<151> PRIOR FILING DATE: 2002-11-13
<150> PRIOR APPLICATION NUMBER: US 60/433,215
<151> PRIOR FILING DATE: 2002-12-12
<150> PRIOR APPLICATION NUMBER: US 60/453,127
<151> PRIOR FILING DATE: 2003-03-07
<150> PRIOR APPLICATION NUMBER: US 60/454,801
<151> PRIOR FILING DATE: 2003-03-13
<150> PRIOR APPLICATION NUMBER: US 60/465,619
<151> PRIOR FILING DATE: 2003-04-24
<150> PRIOR APPLICATION NUMBER: US 60/465,495
<151> PRIOR FILING DATE: 2003-04-24
<150> PRIOR APPLICATION NUMBER: US 60/491,800
<151> PRIOR FILING DATE: 2003-08-01
<160> NUMBER OF SEQ ID NOS: 42
<170> SOFTWARE: PERL Program

<210> SEQ ID NO 1

<211> LENGTH: 114

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<220> FEATURE:

<221> NAME/KEY: misc_feature

<223> OTHER INFORMATION: Incyte ID No: 7511098CD1

<400> SEQUENCE: 1

Met	Lys	Gly	Trp	Gly	Trp	Leu	Ala	Leu	Leu	Leu	Gly	Ala	Leu	Leu
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Gly	Thr	Ala	Trp	Ala	Arg	Arg	Ser	Gln	Asp	Leu	His	Cys	Gly	Ala
														30
Cys	Arg	Ala	Leu	Val	Asp	Glu	Leu	Glu	Trp	Glu	Ile	Ala	Gln	Val
														45
Asp	Pro	Lys	Lys	Thr	Ile	Gln	Met	Gly	Ser	Phe	Arg	Ile	Asn	Pro
														60
Asp	Gly	Ser	Gln	Ser	Val	Val	Glu	Cys	Glu	Ser	Ile	Val	Glu	Glu
														75
Tyr	Glu	Asp	Glu	Leu	Ile	Glu	Phe	Phe	Ser	Arg	Glu	Ala	Asp	Asn
														90
Val	Lys	Asp	Lys	Leu	Cys	Ser	Lys	Arg	Thr	Asp	Leu	Cys	Asp	His
														105
Ala	Leu	His	Ile	Ser	His	Asp	Glu	Leu						
														110

<210> SEQ ID NO 2

<211> LENGTH: 87
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Incyte ID No: 7522037CD1
<400> SEQUENCE: 2

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1				5					10					15
Leu	Gly	Phe	Glu	Val	Gln	Gly	Thr	Gln	Gln	Pro	Gln	Gln	Asp	Glu
				20					25					30
Met	Pro	Ser	Pro	Thr	Phe	Leu	Thr	Gln	Val	Lys	Glu	Ser	Leu	Ser
					35				40					45
Ser	Tyr	Trp	Glu	Ser	Ala	Lys	Thr	Ala	Ala	Gln	Asn	Leu	Asp	Leu
					50				55					60
Tyr	Ser	Lys	Ser	Thr	Ala	Ala	Met	Ser	Thr	Tyr	Thr	Gly	Ile	Phe
					65				70					75
Thr	Asp	Gln	Val	Leu	Ser	Val	Leu	Lys	Gly	Glu	Glu			
					80				85					

<210> SEQ ID NO 3
<211> LENGTH: 248
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Incyte ID No: 7524271CD1
<400> SEQUENCE: 3

Met	Ala	Glu	Ser	His	Leu	Leu	Gln	Trp	Leu	Leu	Leu	Leu	Leu	Pro
1					5				10					15
Thr	Leu	Cys	Gly	Pro	Gly	Thr	Ala	Ala	Trp	Thr	Thr	Ser	Ser	Leu
					20					25				30
Ala	Cys	Ala	Gln	Gly	Pro	Glu	Phe	Trp	Cys	Gln	Ser	Leu	Glu	Gln
					35				40					45
Ala	Leu	Gln	Cys	Arg	Ala	Leu	Gly	His	Cys	Leu	Gln	Glu	Val	Trp
					50				55					60
Gly	His	Val	Gly	Ala	Asp	Leu	Ser	Glu	Gln	Gln	Phe	Pro	Ile	Pro
					65				70					75
Leu	Pro	Tyr	Cys	Trp	Leu	Cys	Arg	Ala	Leu	Ile	Lys	Arg	Ile	Gln
					80				85					90
Ala	Met	Ile	Pro	Lys	Gly	Ala	Leu	Ala	Val	Ala	Val	Ala	Gln	Val
					95				100					105
Cys	Arg	Val	Val	Pro	Leu	Val	Ala	Gly	Gly	Ile	Cys	Gln	Cys	Leu
					110				115					120
Ala	Glu	Arg	Tyr	Ser	Val	Ile	Leu	Leu	Asp	Thr	Leu	Leu	Gly	Arg
					125				130					135
Met	Leu	Pro	Gln	Leu	Val	Cys	Arg	Leu	Val	Leu	Arg	Cys	Ser	Met
					140				145					150
Asp	Asp	Ser	Ala	Gly	Pro	Arg	Glu	Trp	Leu	Pro	Arg	Asp	Ser	Glu
					155				160					165
Cys	His	Leu	Cys	Met	Ser	Val	Thr	Thr	Gln	Ala	Gly	Asn	Ser	Ser
					170				175					180
Glu	Gln	Ala	Ile	Pro	Gln	Ala	Met	Leu	Gln	Ala	Cys	Val	Gly	Ser
					185				190					195
Trp	Leu	Asp	Arg	Glu	Lys	Cys	Lys	Gln	Phe	Val	Glu	Gln	His	Thr
					200				205					210
Pro	Gln	Leu	Leu	Thr	Leu	Val	Pro	Arg	Gly	Trp	Asp	Ala	His	Thr

215 220 225
Thr Cys Gln Ala Leu Gly Val Cys Gly Thr Met Ser Ser Pro Leu
230 235 240
Gln Cys Ile His Ser Pro Asp Leu
245

<210> SEQ ID NO 4

<211> LENGTH: 906

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<220> FEATURE:

<221> NAME/KEY: misc_feature

<223> OTHER INFORMATION: Incyte ID No: 7513132CD1

<400> SEQUENCE: 4

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Ala Pro Ser Asp Ala Glu Val Leu His Leu Cys Arg Ser Leu Glu
20 25 30
Val Gly Thr Val Met Thr Leu Phe Tyr Ser Lys Lys Ser Gln Arg
35 40 45
Pro Glu Arg Lys Thr Phe Gln Val Lys Leu Glu Thr Arg Gln Ile
50 55 60
Thr Trp Ser Arg Gly Ala Asp Lys Ile Glu Gly Ala Ile Asp Ile
65 70 75
Arg Glu Ile Lys Glu Ile Arg Pro Gly Lys Thr Ser Arg Asp Phe
80 85 90
Asp Arg Tyr Gln Glu Asp Pro Ala Phe Arg Pro Asp Gln Ser His
95 100 105
Cys Phe Val Ile Leu Tyr Gly Met Glu Phe Arg Leu Lys Thr Leu
110 115 120
Ser Leu Gln Ala Thr Ser Glu Asp Glu Val Asn Met Trp Ile Lys
125 130 135
Gly Leu Thr Trp Leu Met Glu Asp Thr Leu Gln Ala Pro Thr Pro
140 145 150
Leu Gln Ile Glu Arg Trp Leu Arg Lys Gln Phe Tyr Ser Val Asp
155 160 165
Arg Asn Arg Glu Asp Arg Ile Ser Ala Lys Asp Leu Lys Asn Met
170 175 180
Leu Ser Gln Val Asn Tyr Arg Val Pro Asn Met Arg Phe Leu Arg
185 190 195
Glu Arg Leu Thr Asp Leu Glu Gln Arg Ser Gly Asp Ile Thr Tyr
200 205 210
Gly Gln Phe Ala Gln Leu Tyr Arg Ser Leu Met Tyr Ser Ala Gln
215 220 225
Lys Thr Met Asp Leu Pro Phe Leu Glu Ala Ser Thr Leu Arg Ala
230 235 240
Gly Glu Arg Pro Glu Leu Cys Arg Val Ser Leu Pro Glu Phe Gln
245 250 255
Gln Phe Leu Leu Asp Tyr Gln Gly Glu Leu Trp Ala Val Asp Arg
260 265 270
Leu Gln Val Gln Glu Phe Met Leu Ser Phe Leu Arg Asp Pro Leu
275 280 285
Arg Glu Ile Glu Glu Pro Tyr Phe Phe Leu Asp Glu Phe Val Thr
290 295 300
Phe Leu Phe Ser Lys Glu Asn Ser Val Trp Asn Ser Gln Leu Asp
305 310 315
Ala Val Cys Pro Asp Thr Met Asn Asn Pro Leu Ser His Tyr Trp

320	325	330
Ile Ser Ser Ser His Asn Thr Tyr Leu Thr Gly Asp Gln Phe Ser		
335	340	345
Ser Glu Ser Ser Leu Glu Ala Tyr Ala Arg Cys Leu Arg Met Gly		
350	355	360
Cys Arg Cys Ile Glu Leu Asp Cys Trp Asp Gly Pro Asp Gly Met		
365	370	375
Pro Val Ile Tyr His Gly His Thr Leu Thr Thr Lys Ile Lys Phe		
380	385	390
Ser Asp Val Leu His Thr Ile Lys Glu His Ala Phe Val Ala Ser		
395	400	405
Glu Tyr Pro Val Ile Leu Ser Ile Glu Asp His Cys Ser Ile Ala		
410	415	420
Gln Gln Arg Asn Met Ala Gln Tyr Phe Lys Lys Val Leu Gly Asp		
425	430	435
Thr Leu Leu Thr Lys Pro Val Glu Ile Ser Ala Asp Gly Leu Pro		
440	445	450
Ser Pro Asn Gln Leu Lys Arg Lys Ile Leu Ile Lys His Lys Lys		
455	460	465
Leu Ala Glu Gly Ser Ala Tyr Glu Glu Val Pro Thr Ser Met Met		
470	475	480
Tyr Ser Glu Asn Asp Ile Ser Asn Ser Ile Lys Asn Gly Ile Leu		
485	490	495
Tyr Leu Glu Asp Pro Val Asn His Glu Trp Tyr Pro His Tyr Phe		
500	505	510
Val Leu Thr Ser Ser Lys Ile Tyr Tyr Ser Glu Glu Thr Ser Ser		
515	520	525
Asp Gln Gly Asn Glu Asp Glu Glu Pro Lys Glu Val Ser Ser		
530	535	540
Ser Thr Glu Leu His Ser Asn Glu Lys Trp Phe His Gly Lys Leu		
545	550	555
Gly Ala Gly Arg Asp Gly Arg His Ile Ala Glu Arg Leu Leu Thr		
560	565	570
Glu Tyr Cys Ile Glu Thr Gly Ala Pro Asp Gly Ser Phe Leu Val		
575	580	585
Arg Glu Ser Glu Thr Phe Val Gly Asp Tyr Thr Leu Ser Phe Trp		
590	595	600
Arg Asn Gly Lys Val Gln His Cys Arg Ile His Ser Arg Gln Asp		
605	610	615
Ala Gly Thr Pro Lys Phe Phe Leu Thr Asp Asn Leu Val Phe Asp		
620	625	630
Ser Leu Tyr Asp Leu Ile Thr His Tyr Gln Gln Val Pro Leu Arg		
635	640	645
Cys Asn Glu Phe Glu Met Arg Leu Ser Glu Pro Val Pro Gln Thr		
650	655	660
Asn Ala His Glu Ser Lys Glu Trp Tyr His Ala Ser Leu Thr Arg		
665	670	675
Ala Gln Ala Glu His Met Leu Met Arg Val Pro Arg Asp Gly Ala		
680	685	690
Phe Leu Val Arg Lys Arg Asn Glu Pro Asn Ser Tyr Ala Ile Ser		
695	700	705
Phe Arg Ala Glu Gly Lys Ile Lys His Cys Arg Val Gln Gln Glu		
710	715	720
Gly Gln Thr Val Met Leu Gly Asn Ser Glu Phe Asp Ser Leu Val		
725	730	735
Asp Leu Ile Ser Tyr Tyr Glu Lys His Pro Leu Tyr Arg Lys Met		
740	745	750

Lys Leu Arg Tyr Pro Ile Asn Glu Glu Ala Leu Glu Lys Ile Gly
 755 760 765
 Thr Ala Glu Pro Asp Tyr Gly Ala Leu Tyr Glu Gly Arg Asn Pro
 770 775 780
 Gly Phe Tyr Val Glu Ala Asn Pro Met Pro Thr Phe Lys Cys Ala
 785 790 795
 Val Lys Ala Leu Phe Asp Tyr Lys Ala Gln Arg Glu Asp Glu Leu
 800 805 810
 Thr Phe Ile Lys Ser Ala Ile Ile Gln Asn Val Glu Lys Gln Glu
 815 820 825
 Gly Gly Trp Trp Arg Gly Asp Tyr Gly Gly Lys Lys Gln Leu Trp
 830 835 840
 Phe Pro Ser Asn Tyr Val Glu Glu Met Val Asn Pro Val Ala Leu
 845 850 855
 Glu Pro Glu Arg Glu His Leu Asp Glu Asn Ser Pro Leu Gly Asp
 860 865 870
 Leu Leu Arg Gly Val Leu Asp Val Pro Ala Cys Gln Ile Ala Trp
 875 880 885
 Arg Arg Trp Pro Thr Gly Pro Trp Met Leu Leu Pro Thr His Arg
 890 895 900
 Arg Ser Cys Arg Thr Gly
 905

<210> SEQ ID NO 5
 <211> LENGTH: 1266
 <212> TYPE: PRT
 <213> ORGANISM: Homo sapiens
 <220> FEATURE:
 <221> NAME/KEY: misc_feature
 <223> OTHER INFORMATION: Incyte ID No: 7513134CD1
 <400> SEQUENCE: 5

Met Ala Gly Ala Ala Ser Pro Cys Ala Asn Gly Cys Gly Pro Gly			
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Ala Pro Ser Asp Ala Glu Val Leu His Leu Cys Arg Ser Leu Glu			
20	25	30	
Val Gly Thr Val Met Thr Leu Phe Tyr Ser Lys Lys Ser Gln Arg			
35	40	45	
Pro Glu Arg Lys Thr Phe Gln Val Lys Leu Glu Thr Arg Gln Ile			
50	55	60	
Thr Trp Ser Arg Gly Ala Asp Lys Ile Glu Gly Ala Ile Asp Ile			
65	70	75	
Arg Glu Ile Lys Glu Ile Arg Pro Gly Lys Thr Ser Arg Asp Phe			
80	85	90	
Asp Arg Tyr Gln Glu Asp Pro Ala Phe Arg Pro Asp Gln Ser His			
95	100	105	
Cys Phe Val Ile Leu Tyr Gly Met Glu Phe Arg Leu Lys Thr Leu			
110	115	120	
Ser Leu Gln Ala Thr Ser Glu Asp Glu Val Asn Met Trp Ile Lys			
125	130	135	
Gly Leu Thr Trp Leu Met Glu Asp Thr Leu Gln Ala Pro Thr Pro			
140	145	150	
Leu Gln Ile Glu Arg Trp Leu Arg Lys Gln Phe Tyr Ser Val Asp			
155	160	165	
Arg Asn Arg Glu Asp Arg Ile Ser Ala Lys Asp Leu Lys Asn Met			
170	175	180	
Leu Ser Gln Val Asn Tyr Arg Val Pro Asn Met Arg Phe Leu Arg			
185	190	195	

Glu Arg Leu Thr Asp Leu Glu Gln Arg Ser Gly Asp Ile Thr Tyr
200 205 210
Gly Gln Phe Ala Gln Leu Tyr Arg Ser Leu Met Tyr Ser Ala Gln
215 220 225
Lys Thr Met Asp Leu Pro Phe Leu Glu Ala Ser Thr Leu Arg Ala
230 235 240
Gly Glu Arg Pro Glu Leu Cys Arg Val Ser Leu Pro Glu Phe Gln
245 250 255
Gln Phe Leu Leu Asp Tyr Gln Gly Glu Leu Trp Ala Val Asp Arg
260 265 270
Leu Gln Val Gln Glu Phe Met Leu Ser Phe Leu Arg Asp Pro Leu
275 280 285
Arg Glu Ile Glu Glu Pro Tyr Phe Phe Leu Asp Glu Phe Val Thr
290 295 300
Phe Leu Phe Ser Lys Glu Asn Ser Val Trp Asn Ser Gln Leu Asp
305 310 315
Ala Val Cys Pro Asp Thr Met Asn Asn Pro Leu Ser His Tyr Trp
320 325 330
Ile Ser Ser Ser His Asn Thr Tyr Leu Thr Gly Asp Gln Phe Ser
335 340 345
Ser Glu Ser Ser Leu Glu Ala Tyr Ala Arg Cys Leu Arg Met Gly
350 355 360
Cys Arg Cys Ile Glu Leu Asp Cys Trp Asp Gly Pro Asp Gly Met
365 370 375
Pro Val Ile Tyr His Gly His Thr Leu Thr Thr Lys Ile Lys Phe
380 385 390
Ser Asp Val Leu His Thr Ile Lys Glu His Ala Phe Val Ala Ser
395 400 405
Glu Tyr Pro Val Ile Leu Ser Ile Glu Asp His Cys Ser Ile Ala
410 415 420
Gln Gln Arg Asn Met Ala Gln Tyr Phe Lys Lys Val Leu Gly Asp
425 430 435
Thr Leu Leu Thr Lys Pro Val Glu Ile Ser Ala Asp Gly Leu Pro
440 445 450
Ser Pro Asn Gln Leu Lys Arg Lys Ile Leu Ile Lys His Lys Lys
455 460 465
Leu Ala Glu Gly Ser Ala Tyr Glu Glu Val Pro Thr Ser Met Met
470 475 480
Tyr Ser Glu Asn Asp Ile Ser Asn Ser Ile Lys Asn Gly Ile Leu
485 490 495
Tyr Leu Glu Asp Pro Val Asn His Glu Trp Tyr Pro His Tyr Phe
500 505 510
Val Leu Thr Ser Ser Lys Ile Tyr Tyr